

CLAIMS

1. Nucleotides encoding the full length or part of the nucleocapsid (NP) protein of Newcastle disease virus (NDV).

2. The nucleotides as claimed in claim 1 characterised in that it has the following nucleotide sequence:

	10	20	30	40	50	60
	ATGTCTTCG	TATTCGATGA	ATACGAGCAG	CTCCTCGCTG	CTCAGACTCG	CCCCAATGGA
	70	80	90	100	110	120
	GCTCACGGAG	GGGAGAGAG	AGGGAGCACT	TTAAGAGTTG	AGGTCCCAGT	ATTCACTCTT
10	130	140	150	160	170	180
	AACAGTGACG	ATCCAGAAGA	TAGATGGAAT	TTTGCGGTAT	TCTGTCTTCG	GATTGCTGTT
	190	200	210	220	230	240
	AGCGAGGACG	CCAACAAACC	GCTCAGGCAA	GGTGCTCTCA	TATCCCTCCT	GTGCTCCCAT
15	250	260	270	280	290	300
	TCTCAAGTGA	TGAGGAACCA	TGTTGCCCTT	GCAGGAAAAC	AGAATGAGGC	TACTACTGACT
	310	320	330	340	350	360
	GTTCTTGAGA	TCGATGGTTT	TACCAGCAGC	GTGCCTCAGT	TCAACAACAG	GAGTGGGGTG
	370	380	390	400	410	420
	TCTGAGGAGA	GAGCACAGAG	ATTCATGGTG	ATAGCAGGGT	CTCTCCCTCG	GGCGTGCAGT
20	430	440	450	460	470	480
	AACGGTACTC	CGTTCGTCAC	GGCTGGGGTT	GAAGATGATG	CACCAGAAGA	TATCACTGAT
	490	500	510	520	530	540
	ACTCTGGAAA	GAATCCTGTC	TATCCAGGCT	CAGGTATGGG	TCACAGTAGC	GAAGGCCATG
	550	560	570	580	590	600
25	ACTGCATATG	AGACAGCAGA	TGAGTCGGAA	ACAAGAAGAA	TCAATAAGTA	CATGCAGCAA
	610	620	630	640	650	660
	GGCAGAGTCC	AGAAGAAGTA	CATCCTCCAC	CCTGTATGCA	GGAGTGCAAT	TCAACTCACA
	670	680	690	700	710	720
	ATCAGACATT	CTCTGGCAGT	CCGCATTTTC	TTAGTTAGCG	AGCTTAAGAG	AGGCCGCAAT
30	730	740	750	760	770	780
	ACGGCAGGTG	GGAGCTCCAC	GTATTACAAC	TTAGTAGGGG	ATGTAGACTC	ATACATCAGG
	790	800	810	820	830	840
	AACACCGGAC	TTACTGCATT	CTTCCTTACA	CTCAAATATG	GAATTAATAC	CAAGACATCA

850 860 870 880 890 900
 GCCCTAGCAC TCAGCAGCCT CACAGGCGAT ATCCAAAAGA TGAAGCAGCT CATGCGTTTA
 910 920 930 940 950 960
 TATCGGATGA AGGGAGAAAA TCGCCCGTAC ATGACATTGC TAGGTGACAG TGATCAGATG
 5 970 980 990 1000 1010 1020
 AGCTTTGCAC CGGCTGAGTA TGCACAGCTT TATTCTTTTG CCATGGGCAT GGCATCAGTC
 1030 1040 1050 1060 1070 1080
 TTAGATAAAG GAACTGGCAA ATACCAATTC GCCAGAGACT TCATGAGCAC ATCATTCTGG
 1090 1100 1110 1120 1130 1140
 10 AGACTCGGGG TGGAGTATGC TCAGGCTCAG GGGAGTAGCA TCAACGAAGA CATGGCTGCT
 1150 1160 1170 1180 1190 1200
 GAGCTAA AAC TAACCCCGGC AGCAAGAAGG GGCCTGGCAG CTGCTGCCCA ACGAGTGTCT
 1210 1220 1230 1240 1250 1260
 GAGGAACTG GCAGCGTGGA TATTCCTACT CAACAAGCCG GGGTCCTCAC TGGGCTCAGC
 1270 1280 1290 1300 1310 1320
 15 GATGGAGGCC CCCGAGCCTC TCAGGGTGGA TCGAACAAGT CGCAAGGGCA ACCAGATGCC
 1330 1340 1350 1360 1370 1380
 GGAGATGGGG AGACCCAATT CTTGGATTTG ATGAGAGCAG TGGCGAACAG CATGCGAGAA
 1390 1400 1410 1420 1430 1440
 20 GCGCCAACT CCGCACAGAG CACCACCCAC CCGGAACCCC CCCCAGTCC CGGGCCATCA
 1450 1460 1470 1480 1490 1500
 CAAGATAACG ACACCGACTG GGGGTATTGA

3. Nucleotides encoding the full length or part of the phosphoprotein (P) of Newcastle disease virus (NDV).

25 4. The nucleotides as claimed in claim 3 characterised in that it has the following nucleotide sequence:

10 20 30 40 50 60
 ATGGCCACCT TTACAGATGC GGAGATAGAT GATATATTTG AGACCAGTGG AACTGTCATT
 70 80 90 100 110 120
 30 GACAGCATAA TTACGGCCCA GGGTAAATCA GCAGAGACTG TCGGAAGGAG CGCAATCCCA
 130 140 150 160 170 180
 CAAGGCAAGA CCAAAGCGCT GAGCATAGCA TGGGAGAAGC ATGGGAGCAT CCAACCATCC
 190 200 210 220 230 240
 ACCAGCCAGG ACAACCCCGA CCAACAGGAT AGACCAGACA AACAGCTATC CACACCTGAG
 250 260 270 280 290 300
 35 CAGGCGACCC CACACAACAG CTCGCCAGCC ACATCCGCCG AACCGCTCCC CACTCAGGCC

310 320 330 340 350 360
 GCAGGTGAGG CCGGCGACAC ACAGCTCAAG ACCGGAGCAA GCAACTCTCT TCTGTCTATG
 370 380 390 400 410 420
 CTCGACAAGC TGAGCAATAA ACCATCTAAT GCTAAAAAGG GCCCATGGTC GAGTCCCCAG
 5 430 440 450 460 470 480
 GAAGGATATC ATCAACCTCC GACCCAACAA CATGGGGATC AGCCGAACCG CGGAAACAGC
 490 500 510 520 530 540
 CAGGAGAGGC TCGGGCACCA AGCCAAGGCC GCCCCTGGAA GCCGGGGCAC AGACGCGAGC
 10 550 560 570 580 590 600
 ACAGCATATC ATGGACAATG GAAGGAGTCA CAACTATCAG CTGGTGCAAC CCCTCATGTG
 610 620 630 640 650 660
 CTCCAATCAG GGCAGAGCCA AGACAGTACT CCTGTACCTG TGGATCATGT CCAGCCACCT
 670 680 690 700 710 720
 GTCGACTTTG TGCAGGCGAT GATGACTATG ATGGAGGCGT TATCACAGAA GGTAAGTAAA
 15 730 740 750 760 770 780
 GTCGACTATC AGCTAGACCT AGTCTTAAAG CAGACATCCT CCATCCCTAT GATGCGGTCT
 790 800 810 820 830 840
 GAAATCCAAC AGCTAAAAAC ATCTGTTGCG GTCATGGAAG CTAATTTAGG CATGATGAAA
 20 850 860 870 880 890 900
 ATTCTGGACC CTGGTTGTGC TAACATTTCA TCCTTAAGTG ATCTGCGGGC AGTCGCCCCG
 910 920 930 940 950 960
 TCCCACCCAG TTTTAATTTT AGGCCCCGGA GATCCGTCCC CCTACGTGAC ACAAGGGGGT
 970 980 990 1000 1010 1020
 GAGATGACAC TCAATAAACT CTCACAACCA GTACAACACC CTTCCGAGTT AATTAAATCT
 25 1030 1040 1050 1060 1070 1080
 GCCACAGCGG GCGGACCTGA TATGGGAGTG GAAAAGGACA CTGTCCGTGC ATTGATCACC
 1090 1100 1110 1120 1130 1140
 TCGCGCCCCG TGATCCAAG CTCCTCAGCT AAGCTCCTGA GTAAGCTGGA TGCAGCCGGG
 30 1150 1160 1170 1180 1190 1200
 TCGATTGAAG AGATCAGAAA GATCAAGCGC CTTGCACTAA ATGGCTAA... ..

5. The NP protein coded according to claim 1 or claim 2 characterised in that it has the following amino acid sequence:

1 M S S V F D E Y E Q L L A A Q T 16
 ATG TCT TCC GTA TTC GAT GAA TAC GAG CAG CTC CTC GCT GCT CAG ACT
 1 10 20 30 40
 17 R P N G A H G G G E R G S T L R 32
 CGC CCC AAT GGA GCT CAC GGA GGG GGA GAG AGA GGG AGC ACT TTA AGA
 50 60 70 80 90

5	33	V E V P V F T L N S D D P E D R	48
		GTT GAG GTC CCA GTA TTC ACT CTT AAC AGT GAC GAT CCA GAA GAT AGA	
		100 110 120 130 140	
10	49	W N F A V F C L R I A V S E D A	64
		TGG AAT TTT GCG GTA TTC TGT CTT CGG ATT GCT GTT AGC GAG GAC GCC	
		150 160 170 180 190	
15	65	N K P L R Q G A L I S L L C S H	80
		AAC AAA CCG CTC AGG CAA GGT GCT CTC ATA TCC CTC CTG TGC TCC CAT	
		200 210 220 230 240	
20	81	S Q V M R N H V A L A G K Q N E	96
		TCT CAA GTG ATG AGG AAC CAT GTT GCC CTT GCA GGA AAA CAG AAT GAG	
		250 260 270 280	
25	97	A T L T V L E I D G F T S S V P	112
		GCT ACA CTG ACT GTT CTT GAG ATC GAT GGT TTT ACC AGC AGC GTG CCT	
		290 300 310 320 330	
30	113	Q F N N R S G V S E E R A Q R F	128
		CAG TTC AAC AAC AGG AGT GGG GTG TCT GAG GAG AGA GCA CAG AGA TTC	
		340 350 360 370 380	
35	129	M V I A G S L P R A C S N G T P	144
		ATG GTG ATA GCA GGG TCT CTC CCT CGG GCG TGC AGT AAC GGT ACT CCG	
		390 400 410 420 430	
40	145	F V T A G V E D D A P E D I T D	160
		TTC GTC ACG GCT GGG GTT GAA GAT GAT GCA CCA GAA GAT ATC ACT GAT	
		440 450 460 470 480	
45	161	T L E R I L S I Q A Q V W V T V	176
		ACT CTG GAA AGA ATC CTG TCT ATC CAG GCT CAG GTA TGG GTC ACA GTA	
		490 500 510 520	
50	177	A K A M T A Y E T A D E S E T R	192
		GCG AAG GCC ATG ACT GCA TAT GAG ACA GCA GAT GAG TCG GAA ACA AGA	
		530 540 550 560 570	
55	193	R I N K Y M Q Q G R V Q K K Y I	208
		AGA ATC AAT AAG TAC ATG CAG CAA GGC AGA GTC CAG AAG AAG TAC ATC	
		580 590 600 610 620	
60	209	L H P V C R S A I Q L T I R H S	224
		CTC CAC CCT GTA TGC AGG AGT GCA ATT CAA CTC ACA ATC AGA CAT TCT	
		630 640 650 660 670	
65	225	L A V R I F L V S E L K R G R N	240
		CTG GCA GTC CGC ATT TTC TTA GTT AGC GAG CTT AAG AGA GGC CGC AAT	
		680 690 700 710 720	
70	241	T A G G S S T Y Y N L V G D V D	256
		ACG GCA GGT GGG AGC TCC ACG TAT TAC AAC TTA GTA GGG GAT GTA GAC	
		730 740 750 760	
75	257	S Y I R N T G L T A F F L T L K	272
		TCA TAC ATC AGG AAC ACC GGA CTT ACT GCA TTC TTC CTT ACA CTC AAA	
		770 780 790 800 810	
80	273	Y G I N T K T S A L A L S S L T	288
		TAT GGA ATT AAT ACC AAG ACA TCA GCC CTA GCA CTC AGC AGC CTC ACA	
		820 830 840 850 860	
85	289	G D I Q K M K Q L M R L Y R M K	304
		GGC GAT ATC CAA AAG ATG AAG CAG CTC ATG CGT TTA TAT CGG ATG AAG	
		870 880 890 900 910	

5	305	G E N A P Y M T L L G D S D Q M	320
		GGA GAA AAT GCG CCG TAC ATG ACA TTG CTA GGT GAC AGT GAT CAG ATG	
		920 930 940 950 960	
	321	S F A P A E Y A Q L Y S F A M G	336
		AGC TTT GCA CCG GCT GAG TAT GCA CAG CTT TAT TCT TTT GCC ATG GGC	
10		970 980 990 1000	
	337	M A S V L D K G T G K Y Q F A R	352
		ATG GCA TCA GTC TTA GAT AAA GGA ACT GGC AAA TAC CAA TTC GCC AGA	
		1010 1020 1030 1040 1050	
	353	D F M S T S F W R L G V E Y A Q	368
15		GAC TTC ATG AGC ACA TCA TTC TGG AGA CTC GGG GTG GAG TAT GCT CAG	
		1060 1070 1080 1090 1100	
	369	A Q G S S I N E D M A A E L K L	384
		GCT CAG GGG AGT AGC ATC AAC GAA GAC ATG GCT GCT GAG CTA AAA CTA	
		1110 1120 1130 1140 1150	
20	385	T P A A R R G L A A A A Q R V S	400
		ACC CCG GCA GCA AGA AGG GGC CTG GCA GCT GCT GCC CAA CGA GTG TCT	
		1160 1170 1180 1190 1200	
	401	E E T G S V D I P T Q Q A G V L	416
		GAG GAA ACT GGC AGC GTG GAT ATT CCT ACT CAA CAA GCC GGG GTC CTC	
25		1210 1220 1230 1240	
	417	T G L S D G G P R A S Q G G S N	432
		ACT GGG CTC AGC GAT GGA GGC CCC CGA GCC TCT CAG GGT GGA TCG AAC	
		1250 1260 1270 1280 1290	
	433	K S Q G Q P D A G D G E T Q F L	448
30		AAG TCG CAA GGG CAA CCA GAT GCC GGA GAT GGG GAG ACC CAA TTC TTG	
		1300 1310 1320 1330 1340	
	449	D L M R A V A N S M R E A P N S	464
		GAT TTG ATG AGA GCA GTG GCG AAC AGC ATG CGA GAA GCG CCA AAC TCC	
		1350 1360 1370 1380 1390	
35	465	A Q S T T H P E P P P T P G P S	480
		GCA CAG AGC ACC ACC CAC CCG GAA CCC CCC CCG ACT CCC GGG CCA TCC	
		1400 1410 1420 1430 1440	
	481	Q D N D T D W G Y *	490
		CAA GAT AAC GAC ACC GAC TGG GGG TAT TGA	
		1450 1460 1470	

6. The P protein coded according to claim 3 or claim 4 characterised in that it has the following amino acid sequence:

40	1	M A T F T D A E I D D I F E T S	16
		ATG GCC ACC TTT ACA GAT GCG GAG ATA GAT GAT ATA TTT GAG ACC AGT	
45	17	G T V I D S I I T A Q G K S A E	32
		GGA ACT GTC ATT GAC AGC ATA ATT ACG GCC CAG GGT AAA TCA GCA GAG	
		50 60 70 80 90	

5	33	T	V	G	R	S	A	I	P	Q	G	K	T	K	A	L	S	48
		ACT	GTC	GGA	AGG	AGC	GCA	ATC	CCA	CAA	GGC	AAG	ACC	AAA	GCG	CTG	AGC	
		100				110			120			130			140			
10	49	I	A	W	E	K	H	G	S	I	Q	P	S	T	S	Q	D	64
		ATA	GCA	TGG	GAG	AAG	CAT	GGG	AGC	ATC	CAA	CCA	TCC	ACC	AGC	CAG	GAC	
		150				160			170			180			190			
15	65	N	P	D	Q	Q	D	R	P	D	K	Q	L	S	T	P	E	80
		AAC	CCC	GAC	CAA	CAG	GAT	AGA	CCA	GAC	AAA	CAG	CTA	TCC	ACA	CCT	GAG	
		200				210			220			230			240			
20	81	Q	A	T	P	H	N	S	S	P	A	T	S	A	E	P	L	96
		CAG	GCG	ACC	CCA	CAC	AAC	AGC	TCG	CCA	GCC	ACA	TCC	GCC	GAA	CCG	CTC	
		250				260			270			280						
25	97	P	T	Q	A	A	G	E	A	G	D	T	Q	L	K	T	G	112
		CCC	ACT	CAG	GCC	GCA	GGT	GAG	GCC	GGC	GAC	ACA	CAG	CTC	AAG	ACC	GGA	
		290			300			310			320			330				
30	113	A	S	N	S	L	L	S	M	L	D	K	L	S	N	K	P	128
		GCA	AGC	AAC	TCT	CTT	CTG	TCT	ATG	CTC	GAC	AAG	CTG	AGC	AAT	AAA	CCA	
		340			350			360			370			380				
35	129	S	N	A	K	K	G	P	W	S	S	P	Q	E	G	Y	H	144
		TCT	AAT	GCT	AAA	AAG	GGC	CCA	TGG	TCG	AGT	CCC	CAG	GAA	GGA	TAT	CAT	
		390			400			410			420			430				
40	145	Q	P	P	T	Q	Q	H	G	D	Q	P	N	R	G	N	S	160
		CAA	CCT	CCG	ACC	CAA	CAA	CAT	GGG	GAT	CAG	CCG	AAC	CGC	GGA	AAC	AGC	
		440			450			460			470			480				
45	161	Q	E	R	L	R	H	Q	A	K	A	A	P	G	S	R	G	176
		CAG	GAG	AGG	CTG	CGG	CAC	CAA	GCC	AAG	GCC	GCC	CCT	GGA	AGC	CGG	GGC	
		490			500			510			520			530				
50	177	T	D	A	S	T	A	Y	H	G	Q	W	K	E	S	Q	L	192
		ACA	GAC	GCG	AGC	ACA	GCA	TAT	CAT	GGA	CAA	TGG	AAG	GAG	TCA	CAA	CTA	
		530			540			550			560			570				
55	193	S	A	G	A	T	P	H	V	L	Q	S	G	Q	S	Q	D	208
		TCA	GCT	GGT	GCA	ACC	CCT	CAT	GTG	CTC	CAA	TCA	GGG	CAG	AGC	CAA	GAC	
		580			590			600			610			620				
60	209	S	T	P	V	P	V	D	H	V	Q	P	P	V	D	F	V	224
		AGT	ACT	CCT	GTA	CCT	GTG	GAT	CAT	GTC	CAG	CCA	CCT	GTC	GAC	TTT	GTG	
		630			640			650			660			670				
65	225	Q	A	M	M	T	M	M	E	A	L	S	Q	K	V	S	K	240
		CAG	GCG	ATG	ATG	ACT	ATG	ATG	GAG	GCG	TTA	TCA	CAG	AAG	GTA	AGT	AAA	
		680			690			700			710			720				
70	241	V	D	Y	Q	L	D	L	V	L	K	Q	T	S	S	I	P	256
		GTC	GAC	TAT	CAG	CTA	GAC	CTA	GTC	TTA	AAG	CAG	ACA	TCC	TCC	ATC	CCT	
		730			740			750			760			770				
75	257	M	M	R	S	E	I	Q	Q	L	K	T	S	V	A	V	M	272
		ATG	ATG	CGG	TCT	GAA	ATC	CAA	CAG	CTA	AAA	ACA	TCT	GTT	GCG	GTC	ATG	
		770			780			790			800			810				
80	273	E	A	N	L	G	M	M	K	I	L	D	P	G	C	A	N	288
		GAA	GCT	AAT	TTA	GGC	ATG	ATG	AAA	ATT	CTG	GAC	CCT	GGT	TGT	GCT	AAC	
		820			830			840			850			860				
85	289	I	S	S	L	S	D	L	R	A	V	A	R	S	H	P	V	304
		ATT	TCA	TCC	TTA	AGT	GAT	CTG	CGG	GCA	GTC	GCC	CGG	TCC	CAC	CCA	GTT	
		870			880			890			900			910				

305 L I S G P G D P S P Y V T Q G G 320
 TTA ATT TCA GGC CCC GGA GAT CCG TCC CCC TAC GTG ACA CAA GGG GGT
 920 930 940 950 960
 5 321 E M T L N K L S Q P V Q H P S E 336
 GAG ATG ACA CTC AAT AAA CTC TCA CAA CCA GTA CAA CAC CCT TCC GAG
 970 980 990 1000
 337 L I K S A T A G G P D M G V E K 352
 TTA ATT AAA TCT GCC ACA GCG GGC GGA CCT GAT ATG GGA GTG GAA AAG
 1010 1020 1030 1040 1050
 10 353 D T V R A L I T S R P M H P S S 368
 GAC ACT GTC CGT GCA TTG ATC ACC TCG CGC CCG ATG CAT CCA AGC TCC
 1060 1070 1080 1090 1100
 369 S A K L L S K L D A A G S I E E 384
 TCA GCT AAG CTC CTG AGT AAG CTG GAT GCA GCC GGG TCG ATT GAA GAG
 1110 1120 1130 1140 1150
 15 385 I R K I K R L A L N G * 396
 ATC AGA AAG ATC AAG CGC CTT GCA CTA AAT GGC TAA
 1160 1170 1180

7. A recombinant expression plasmid containing the NDV nucleocapsid gene as claimed in claim 1 or claim 2.

8. A recombinant expression plasmid containing the NDV phosphoprotein gene as claimed in claim 3 or claim 4.

9. The recombinant expression plasmid according to claim 7 which is the expression plasmid pTrcHis2-NP constructed by cloning the NDV nucleocapsid gene of claims 1 or 2 into vector pTrcHis2.

10. The recombinant expression plasmid according to claim 8 which is the expression plasmid pTrcHis2-P constructed by cloning the NDV phosphoprotein gene of claims 3 or 4 into vector pTrcHis2.

11. A transformed *Escherichia coli* with the recombinant expression plasmid according to claim 7 or claim 9.

12. A transformed *Escherichia coli* with the recombinant expression plasmid according to claim 8 or claim 10.

13. The transformed microorganism according to claim 11, which is the transformed *E. coli* TOP10 (pTrcHis2-NP) produced by introducing the recombinant expression plasmid of claim 7 or claim 9 into *E. coli* TOP10.

14. The transformed microorganism according to claim 12, which is the transformed *E. coli* (pTrcHis2-P) produced by introducing the recombinant expression plasmid of claim 8 or claim 10 into *E. coli* TOP 10.

15. A fused or non-fused form of NDV nucleocapsid protein isolated and purified from culture of the transformed microorganism of claim 11 or claim 13 characterised in that it has the following amino acid sequence:

10	1	M	S	S	V	F	D	E	Y	E	Q	L	L	A	A	Q	T	16
		ATG	TCT	TCC	GTA	TTC	GAT	GAA	TAC	GAG	CAG	CTC	CTC	GCT	GCT	CAG	ACT	
		1			10			20			30			40				
15	17	R	P	N	G	A	H	G	G	G	E	R	G	S	T	L	R	32
		CGC	CCC	AAT	GGA	GCT	CAC	GGA	GGG	GGA	GAG	AGA	GGG	AGC	ACT	TTA	AGA	
		50			60			70			80			90				
	33	V	E	V	P	V	F	T	L	N	S	D	D	P	E	D	R	48
		GTT	GAG	GTC	CCA	GTA	TTC	ACT	CTT	AAC	AGT	GAC	GAT	CCA	GAA	GAT	AGA	
		100			110			120			130			140				
20	49	W	N	F	A	V	F	C	L	R	I	A	V	S	E	D	A	64
		TGG	AAT	TTT	GCG	GTA	TTC	TGT	CTT	CGG	ATT	GCT	GTT	AGC	GAG	GAC	GCC	
		150			160			170			180			190				
	65	N	K	P	L	R	Q	G	A	L	I	S	L	L	C	S	H	80
		AAC	AAA	CCG	CTC	AGG	CAA	GGT	GCT	CTC	ATA	TCC	CTC	CTG	TGC	TCC	CAT	
			200			210			220			230			240			
25	81	S	Q	V	M	R	N	H	V	A	L	A	G	K	Q	N	E	96
		TCT	CAA	GTG	ATG	AGG	AAC	CAT	GTT	GCC	CTT	GCA	GGA	AAA	CAG	AAT	GAG	
			250			260			270			280						
30	97	A	T	L	T	V	L	E	I	D	G	F	T	S	S	V	P	112
		GCT	ACA	CTG	ACT	GTT	CTT	GAG	ATC	GAT	GGT	TTT	ACC	AGC	AGC	GTG	CCT	
		290			300			310			320			330				
	113	Q	F	N	N	R	S	G	V	S	E	E	R	A	Q	R	F	128
		CAG	TTC	AAC	AAC	AGG	AGT	GGG	GTG	TCT	GAG	GAG	AGA	GCA	CAG	AGA	TTC	
		340			350			360			370			380				
35	129	M	V	I	A	G	S	L	P	R	A	C	S	N	G	T	P	144
		ATG	GTG	ATA	GCA	GGG	TCT	CTC	CCT	CGG	GCG	TGC	AGT	AAC	GGT	ACT	CCG	
		390			400			410			420			430				
	145	F	V	T	A	G	V	E	D	D	A	P	E	D	I	T	D	160
		TTC	GTC	ACG	GCT	GGG	GTT	GAA	GAT	GAT	GCA	CCA	GAA	GAT	ATC	ACT	GAT	
			440			450			460			470			480			
40	161	T	L	E	R	I	L	S	I	Q	A	Q	V	W	V	T	V	176
		ACT	CTG	GAA	AGA	ATC	CTG	TCT	ATC	CAG	GCT	CAG	GTA	TGG	GTC	ACA	GTA	
			490			500			510			520						

5	177	A	K	A	M	T	A	Y	E	T	A	D	E	S	E	T	R	192
		GCG	AAG	GCC	ATG	ACT	GCA	TAT	GAG	ACA	GCA	GAT	GAG	TCG	GAA	ACA	AGA	
		530			540			550			560			570				
10	193	R	I	N	K	Y	M	Q	Q	G	R	V	Q	K	K	Y	I	208
		AGA	ATC	AAT	AAG	TAC	ATG	CAG	CAA	GGC	AGA	GTC	CAG	AAG	AAG	TAC	ATC	
		580			590			600				610			620			
15	209	L	H	P	V	C	R	S	A	I	Q	L	T	I	R	H	S	224
		CTC	CAC	CCT	GTA	TGC	AGG	AGT	GCA	ATT	CAA	CTC	ACA	ATC	AGA	CAT	TCT	
		630			640			650				660			670			
20	225	L	A	V	R	I	F	L	V	S	E	L	K	R	G	R	N	240
		CTG	GCA	GTC	CGC	ATT	TTC	TTA	GTT	AGC	GAG	CTT	AAG	AGA	GGC	CGC	AAT	
			680			690			700			710			720			
25	241	T	A	G	G	S	S	T	Y	Y	N	L	V	G	D	V	D	256
		ACG	GCA	GGT	GGG	AGC	TCC	ACG	TAT	TAC	AAC	TTA	GTA	GGG	GAT	GTA	GAC	
				730			740				750			760				
30	257	S	Y	I	R	N	T	G	L	T	A	F	F	L	T	L	K	272
		TCA	TAC	ATC	AGG	AAC	ACC	GGA	CTT	ACT	GCA	TTC	TTC	CTT	ACA	CTC	AAA	
		770			780			790				800			810			
35	273	Y	G	I	N	T	K	T	S	A	L	A	L	S	S	L	T	288
		TAT	GGA	ATT	AAT	ACC	AAG	ACA	TCA	GCC	CTA	GCA	CTC	AGC	AGC	CTC	ACA	
			820			830			840				850			860		
40	289	G	D	I	Q	K	M	K	Q	L	M	R	L	Y	R	M	K	304
		GGC	GAT	ATC	CAA	AAG	ATG	AAG	CAG	CTC	ATG	CGT	TTA	TAT	CGG	ATG	AAG	
			870			880			890				900			910		
45	305	G	E	N	A	P	Y	M	T	L	L	G	D	S	D	Q	M	320
		GGA	GAA	AAT	GCG	CCG	TAC	ATG	ACA	TTG	CTA	GGT	GAC	AGT	GAT	CAG	ATG	
			920			930			940				950			960		
50	321	S	F	A	P	A	E	Y	A	Q	L	Y	S	F	A	M	G	336
		AGC	TTT	GCA	CCG	GCT	GAG	TAT	GCA	CAG	CTT	TAT	TCT	TTT	GCC	ATG	GGC	
				970			980				990			1000				
55	337	M	A	S	V	L	D	K	G	T	G	K	Y	Q	F	A	R	352
		ATG	GCA	TCA	GTC	TTA	GAT	AAA	GGA	ACT	GGC	AAA	TAC	CAA	TTC	GCC	AGA	
		1010			1020			1030				1040			1050			
60	353	D	F	M	S	T	S	F	W	R	L	G	V	E	Y	A	Q	368
		GAC	TTC	ATG	AGC	ACA	TCA	TTC	TGG	AGA	CTC	GGG	GTG	GAG	TAT	GCT	CAG	
			1060			1070			1080				1090			1100		
65	369	A	Q	G	S	S	I	N	E	D	M	A	A	E	L	K	L	384
		GCT	CAG	GGG	AGT	AGC	ATC	AAC	GAA	GAC	ATG	GCT	GCT	GAG	CTA	AAA	CTA	
			1110			1120			1130				1140			1150		
70	385	T	P	A	A	R	R	G	L	A	A	A	A	Q	R	V	S	400
		ACC	CCG	GCA	GCA	AGA	AGG	GGC	CTG	GCA	GCT	GCT	GCC	CAA	CGA	GTG	TCT	
			1160			1170			1180				1190			1200		
75	401	E	E	T	G	S	V	D	I	P	T	Q	Q	A	G	V	L	416
		GAG	GAA	ACT	GGC	AGC	GTG	GAT	ATT	CCT	ACT	CAA	CAA	GCC	GGG	GTC	CTC	
				1210			1220			1230				1240				
80	417	T	G	L	S	D	G	G	P	R	A	S	Q	G	G	S	N	432
		ACT	GGG	CTC	AGC	GAT	GGA	GGC	CCC	CGA	GCC	TCT	CAG	GGT	GGA	TCG	AAC	
		1250			1260			1270				1280			1290			
85	433	K	S	Q	G	Q	P	D	A	G	D	G	E	T	Q	F	L	448
		AAG	TCG	CAA	GGG	CAA	CCA	GAT	GCC	GGA	GAT	GGG	GAG	ACC	CAA	TTC	TTG	
		1300			1310			1320				1330			1340			

449 D L M R A V A N S M R E A P N S 464
 GAT TTG ATG AGA GCA GTG GCG AAC AGC ATG CGA GAA GCG CCA AAC TCC
 1350 1360 1370 1380 1390

5 465 A Q S T T H P E P P P T P G P S 480
 GCA CAG AGC ACC ACC CAC CCG GAA CCC CCC CCG ACT CCC GGG CCA TCC
 1400 1410 1420 1430 1440

481 Q D N D T D W G Y * 490
 CAA GAT AAC GAC ACC GAC TGG GGG TAT TGA
 1450 1460 1470

10

16. A fused or non-fused form of NDV phosphoprotein isolated and purified from culture of the transformed microorganism of claim 12 or claim 14 characterised in that it has the following amino acid sequence:

15

1 M A T F T D A E I D D I F E T S 16
 ATG GCC ACC TTT ACA GAT GCG GAG ATA GAT GAT ATA TTT GAG ACC AGT
 1 10 20 30 40

17 G T V I D S I I T A Q G K S A E 32
 GGA ACT GTC ATT GAC AGC ATA ATT ACG GCC CAG GGT AAA TCA GCA GAG
 50 60 70 80 90

20 33 T V G R S A I P Q G K T K A L S 48
 ACT GTC GGA AGG AGC GCA ATC CCA CAA GGC AAG ACC AAA GCG CTG AGC
 100 110 120 130 140

49 I A W E K H G S I Q P S T S Q D 64
 ATA GCA TGG GAG AAG CAT GGG AGC ATC CAA CCA TCC ACC AGC CAG GAC
 150 160 170 180 190

25 65 N P D Q Q D R P D K Q L S T P E 80
 AAC CCC GAC CAA CAG GAT AGA CCA GAC AAA CAG CTA TCC ACA CCT GAG
 200 210 220 230 240

30 81 Q A T P H N S S P A T S A E P L 96
 CAG GCG ACC CCA CAC AAC AGC TCG CCA GCC ACA TCC GCC GAA CCG CTC
 250 260 270 280

97 P T Q A A G E A G D T Q L K T G 112
 CCC ACT CAG GCC GCA GGT GAG GCC GGC GAC ACA CAG CTC AAG ACC GGA
 290 300 310 320 330

35 113 A S N S L L S M L D K L S N K P 128
 GCA AGC AAC TCT CTT CTG TCT ATG CTC GAC AAG CTG AGC AAT AAA CCA
 340 350 360 370 380

129 S N A K K G P W S S P Q E G Y H 144
 TCT AAT GCT AAA AAG GGC CCA TGG TCG AGT CCC CAG GAA GGA TAT CAT
 390 400 410 420 430

40 145 Q P P T Q Q H G D Q P N R G N S 160
 CAA CCT CCG ACC CAA CAT GGG GAT CAG CCG AAC CGC GGA AAC AGC
 440 450 460 470 480

161 Q E R L R H Q A K A A P G S R G 176
 CAG GAG AGG CTG CGG CAC CAA GCC AAG GCC GCC CCT GGA AGC CGG GGC
 490 500 510 520

5	177	T	D	A	S	T	A	Y	H	G	Q	W	K	E	S	Q	L	192
		ACA	GAC	GCG	AGC	ACA	GCA	TAT	CAT	GGA	CAA	TGG	AAG	GAG	TCA	CAA	CTA	
	530				540			550			560			570				
10	193	S	A	G	A	T	P	H	V	L	Q	S	G	Q	S	Q	D	208
		TCA	GCT	GGT	GCA	ACC	CCT	CAT	GTG	CTC	CAA	TCA	GGG	CAG	AGC	CAA	GAC	
	580				590			600			610			620				
15	209	S	T	P	V	P	V	D	H	V	Q	P	P	V	D	F	V	224
		AGT	ACT	CCT	GTA	CCT	GTG	GAT	CAT	GTC	CAG	CCA	CCT	GTC	GAC	TTT	GTG	
	630				640			650			660			670				
20	225	Q	A	M	M	T	M	M	E	A	L	S	Q	K	V	S	K	240
		CAG	GCG	ATG	ATG	ACT	ATG	ATG	GAG	GCG	TTA	TCA	CAG	AAG	GTA	AGT	AAA	
	680				690			700			710			720				
25	241	V	D	Y	Q	L	D	L	V	L	K	Q	T	S	S	I	P	256
		GTC	GAC	TAT	CAG	CTA	GAC	CTA	GTC	TTA	AAG	CAG	ACA	TCC	TCC	ATC	CCT	
	730				740			750			760							
30	257	M	M	R	S	E	I	Q	Q	L	K	T	S	V	A	V	M	272
		ATG	ATG	CGG	TCT	GAA	ATC	CAA	CAG	CTA	AAA	ACA	TCT	GTT	GCG	GTC	ATG	
	770				780			790			800			810				
35	273	E	A	N	L	G	M	M	K	I	L	D	P	G	C	A	N	288
		GAA	GCT	AAT	TTA	GGC	ATG	ATG	AAA	ATT	CTG	GAC	CCT	GGT	TGT	GCT	AAC	
	820				830			840			850			860				
40	289	I	S	S	L	S	D	L	R	A	V	A	R	S	H	P	V	304
		ATT	TCA	TCC	TTA	AGT	GAT	CTG	CGG	GCA	GTC	GCC	CGG	TCC	CAC	CCA	GTT	
	870				880			890			900			910				
45	305	L	I	S	G	P	G	D	P	S	P	Y	V	T	Q	G	G	320
		TTA	ATT	TCA	GGC	CCC	GGA	GAT	CCG	TCC	CCC	TAC	GTG	ACA	CAA	GGG	GGT	
	920				930			940			950			960				
50	321	E	M	T	L	N	K	L	S	Q	P	V	Q	H	P	S	E	336
		GAG	ATG	ACA	CTC	AAT	AAA	CTC	TCA	CAA	CCA	GTA	CAA	CAC	CCT	TCC	GAG	
	970				980			990			1000							
55	337	L	I	K	S	A	T	A	G	G	P	D	M	G	V	E	K	352
		TTA	ATT	AAA	TCT	GCC	ACA	GCG	GGC	GGA	CCT	GAT	ATG	GGA	GTG	GAA	AAG	
	1010				1020			1030			1040			1050				
60	353	D	T	V	R	A	L	I	T	S	R	P	M	H	P	S	S	368
		GAC	ACT	GTC	CGT	GCA	TTG	ATC	ACC	TCG	CGC	CCG	ATG	CAT	CCA	AGC	TCC	
	1060				1070			1080			1090			1100				
65	369	S	A	K	L	L	S	K	L	D	A	A	G	S	I	E	E	384
		TCA	GCT	AAG	CTC	CTG	AGT	AAG	CTG	GAT	GCA	GCC	GGG	TCG	ATT	GAA	GAG	
	1110																	